



Lexicon Genetics Incorporated – Genentech Project Materials

Genentech ID:	UNQ606	Date of Submission:	10/19/05
Lexicon Contract Name:	DNA097	Mutation Type:	☒ Standard Knock out
LexVision Name:	MEM671N1		☐ Conditional
Reference accessions:	NM_007962	Is this gene X-linked?	No

Required Materials: ☒ pKOS clone DNA(s) __pKOS-16_____
☒ Target Vector DNA __pKOS-16 TV_____
☒ Targeted ES Cell DNA __1A4_____
☒ Genomic Map

Southern Blot Analysis: *External/Internal Probe Strategies*

	<u>5' External</u>	<u>3' External</u>
Name of Probe:	24/25	30/31
Restriction Enzyme for Genomic Digest:	BglII	XbaI
Predicted Wild-type Band (kb):	10.6 kb	11.8 kb
Predicted Mutant Band (kb):	14.1 kb	13.6 kb
Probe Size:	439 bp	598 bp

PCR Strategies:*For standard knockouts, give wildtype and mutant-specific strategies**For conditionals, give 5' loxP and cre-excision strategies*

Wild type-specific (absent in targeted allele)		Mutation-specific product (absent in wt)	
5' Primer Name:	DNA097-5	5' Primer Name:	Neo3A
3' Primer Name:	DNA097-6	3' Primer Name:	DNA097-17
Predicted Wild-type Band (bp):	358	Predicted Wild-type Band (bp):	none
Predicted mutant band (bp)	none	Predicted mutant band (bp)	408

5' loxP strategy		Distinguish Cre-excised and wt	
5' Primer Name:		5' Primer Name:	
3' Primer Name:		3' Primer Name:	
Predicted Wild-type Band (bp):		Predicted Wild-type Band (bp):	
Predicted mutant band (bp)		Predicted mutant band (bp)	

Primer sequences:**Southern probes**

DNA097-24 5' – TTTCTTTGGGAAATGAATGGAT
 DNA097-25 5' – GTCTAGTCTTGGTCTGAGGCTAGG
 DNA097-30 5' – TTATAAGAATCCCCTAGAACTGTT
 DNA097-31 5' – CTAAATATGACCCTTACCTCGAA

PCR Genotyping

DNA097-5 5' – TCTGAAATTGGTGCGGTAAG
 DNA097-6 5' – GAGGTCGGAAATTCCACGTCACAG
 DNA097-17 5' – GGCTGTGCCTAGCACACCAGGTAC
 Neo3A 5' – GCAGCGCATCGCCTTCTATC

Genomic Sequence Deleted:

ATGTATGCGCAAGAGCCCCGCGCTTGTGCTTCCACTTCTCCTGAGTTTACAGCTCACAGGTAAGAAGTGGCGGGCTTCTA
GGATTTTCTACCATTTGCCGCCATTCTGTAAAGACAGAGCTCATGGCTTGAAGAAATCTCAAGGGCTCCGTTGGGAGAT
CGTGCCCCAACTGCAATTCGTTCTAGTCCAGACTTCGCCGAAACTTCAGTTCGGTGGGTGCTTTGGGGCAGTACTTTGG
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GCACGCACGCACGCCATCCTTTGTGAAGCTGGATGGGAGAGGAGGAAAG

Genomic Locus: *(The deleted sequence represents nt13413-15202-in the sequence below. KOS16 used to generate the TV represents nt9374-18001 in the sequence below.)*

[illegible]

[illegible]

CAAGTTATCTTCAAAGACGACCTATCTCTCCACCCTGTGCATCCGTCTAACTTCCTTCAGGAGTAAGTGAAAGGTTAAA
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Selection Cassette:

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Targeted Locus:

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